

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 27, 2002, 15:34:44 ; Search time 15.93 Seconds

(without alignments)
1898.367 Million cell updates/sec

Title: US-08-774-104A-2

Perfect score: 397

Sequence: 1 MMVFHETRALAQSDIQQLYA.....ETGLKPEPMQLKDYNHVE 397

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 8

Total number of hits satisfying chosen parameters: 30

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	2.5	511	2	T36306
2	10	2.5	523	2	A42301
3	10	2.5	526	2	T49199
4	10	2.5	613	2	T50834
5	9	2.3	396	1	A40365
6	9	2.3	404	2	D86716
7	9	2.3	411	2	B69450
8	9	2.3	433	2	T43924
9	9	2.3	434	2	A75163
10	9	2.3	462	2	S03316
11	9	2.3	471	1	A69657
12	9	2.3	485	2	S75655
13	9	2.3	494	2	E70352
14	9	2.3	494	2	JX0065
15	9	2.3	502	2	C83857
16	9	2.3	508	2	S19266
17	9	2.3	508	2	S74537
18	9	2.3	512	2	JH0098
19	9	2.3	515	1	NMBS1
20	9	2.3	621	2	S27752
21	9	2.3	621	2	JQ1685
22	9	2.0	141	2	E83345
23	8	2.0	387	2	H96552
24	8	2.0	391	1	SYECIK
25	8	2.0	391	2	D85558
26	8	2.0	395	2	A83283
27	8	2.0	430	2	E64059
28	8	2.0	441	2	G82612
29	8	2.0	474	2	B64434

30 8 2.0 616 2 T01990

anthranilate synth

ALIGNMENTS

RESULT 1

T36306

probable anthranilate synthase component I - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000

C:Accession: T36306

R:Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, I

submitted to the EMBL Data Library, March 1999

A:Reference number: Z21604

A:Accession: T36306

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-511 <SAU>

A:Cross-references: EMBL:AL035654; PIDN:CAR38585.1; GSPDB:GN00070; SCOEDB:SCE8.07c

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: trpE2; SCOEDB:SCE8.07c

C:Superfamily: anthranilate synthase component I

Query Match

2.5%; Score 10; DB 2; Length 511;

Best Local Similarity 100.0%; Pred. No. 0.082;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADSD 371

DB 476 AGAGIVADSD 485

RESULT 2

A42301

anthranilate synthase (EC 4.1.3.27) alpha chain - Haloferax volcanii

C:Species: Haloferax volcanii

C>Date: 10-Jul-1992 #sequence_revision 18-Sep-1992 #text_change 22-Jun-1999

C:Accession: A42301

R:Lam, W.L.; Logan, S.M.; Doolittle, W.F.

J. Bacteriol. 174, 1694-1697, 1992

A:Title: Genes for tryptophan biosynthesis in the halophilic archaeobacterium Haloferax

A:Reference number: A42301; M01D:92165748

A:Accession: A42301

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-523 <LAM>

A:Cross-references: GB:M83788; NID:G149036; PIDN:AA73177.1; PID:G149039

A>Note: the authors failed to give the translation for ACC in residue 239 as shown in

C:Superfamily: anthranilate synthase component I

C:Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match

2.5%; Score 10; DB 2; Length 523;

Best Local Similarity 100.0%; Pred. No. 0.084;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADSD 371

DB 483 AGAGIVADSD 492

RESULT 3

T49199

anthranilate synthase alpha-1 chain-like protein - Arabidopsis thaliana

N:Alternate names: protein F27K19.50

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000

C:Accession: T49199

R:Benes, V.; Wurmback, E.; Drzonek, H.; Ansoorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z25014
 A:Accession: T49199
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-526 <BEN>
 A:Cross-references: EMBL:AL163832; GSPDB:GN00061; ATSP:F27K19.50
 A:Experimental source: cultivar Columbia; BAC clone F27K19
 C:Genetics:
 A:Gene: ATSP:F27K19.50
 A:Map position: 3
 A:Insertions: 58/3; 122/1; 172/3; 211/2; 293/3; 312/3; 363/3; 390/3; 413/3
 C:Superfamily: anthranilate synthase component I

Query Match 2.5%; Score 10; DB 2; Length 526;
 Best Local Similarity 100.0%; Pred. No. 0.085;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADSD 371
 DB 483 AGAGIVADSD 492

RESULT 4
 T50834
 anthranilate synthase (PC 4.1.3.27) alpha chain [Imported] - Ruta graveolens
 C:Species: Ruta graveolens
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
 C:Accession: T50834
 R:Bohlmann, J.; Deluca, V.; Ellert, U.; Martin, W.
 Plant J. 7, 491-501, 1995
 A:Title: Purification and cDNA cloning of anthranilate synthase from Ruta graveolens: mc
 A:Reference number: Z25253; MUID:95276783
 A:Accession: T50834
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-613 <BOH>
 A:Cross-references: EMBL:L34344; PIDN:AAA74901.1
 C:Function: <TBS>
 A:Pathway: tryptophan biosynthesis
 C:Function: <AAS>
 A:Pathway: biosynthesis of acridone alkaloids
 C:Superfamily: anthranilate synthase component I
 C:Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match 2.5%; Score 10; DB 2; Length 613;
 Best Local Similarity 100.0%; Pred. No. 0.097;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADSD 371
 DB 572 AGAGIVADSD 581

RESULT 5
 A40365
 siderophore biosynthetic protein amoA - Aeromonas hydrophila
 C:Species: Aeromonas hydrophila
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A40365
 R:Barghouti, S.; Payne, S.M.; Arceneaux, J.E.L.; Byers, B.R.
 J. Bacteriol. 173, 5121-5128, 1991
 A:Title: Cloning, mutagenesis, and nucleotide sequence of a siderophore biosynthetic ge
 A:Reference number: A40365; MUID:91317731
 A:Accession: A40365
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-396 <BAR>
 A:Cross-references: GB:M63339
 A:Note: the authors translated the codon GAG for residue 393 as Gly
 C:Superfamily: Isochorismate synthase

Query Match 2.3%; Score 9; DB 1; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 LFAGAGIVA 368
 DB 358 LFAGAGIVA 366

RESULT 6
 D86716
 hypothetical protein menF [Imported] - Lactococcus lactis subsp. lactis (strain IL140
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
 C:Accession: D86716
 R:Boletijn, A.; Mincker, P.; Manger, S.; Jallion, O.; Malarne, K.; Weissenbach, J.; Eh
 Genome Res. In press, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium.
 A:Reference number: A86625
 A:Accession: D86716
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-404 <SNO>
 A:Cross-references: GB:AE005176; NID:g12723645; PIDN:AAK04830.1; GSPDB:GN00146
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: menF

Query Match 2.3%; Score 9; DB 2; Length 404;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 LHPTPALGG 306
 DB 314 LHPTPALGG 322

RESULT 7
 B69450
 anthranilate synthase component I (trpE) homolog - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Jun-1999
 C:Accession: B69450
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
 Glodex, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kalne, B.P.; Sykes,
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
 A:Reference number: A69250; MUID:98049343
 A:Accession: B69450
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-411 <KLE>
 A:Cross-references: GB:AE000992; GB:AE000782; NID:g2689315; PIDN:AAB89646.1; PID:g264
 C:Superfamily: anthranilate synthase component I

Query Match 2.3%; Score 9; DB 2; Length 411;
 Best Local Similarity 100.0%; Pred. No. 0.72;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
 DB 381 AGAGIVADS 389

RESULT 8
 T43924
 anthranilate synthase component I [Imported] - Pyrococcus kodakarensis

C:Species: *Pyrococcus kodakarensis*
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
 C:Accession: T43924
 R:Imanaka, T.; Ezaki, S.; Atomi, H.
 A:Submitted to the EMBL Data Library, July 1999
 A:Description: trp operon of *Pyrococcus kodakarensis* KOD1.
 A:Reference number: 222725
 A:Accession: T43924
 A:Status: preliminary; translated from GB/EMBL/DDJ
 A:Molecule type: DNA
 A:Residues: 1-433 <IMA>
 A:Cross-references: EMBL:AB030011; PIDN:BAA82547.1
 A:Experimental source: strain KOD1
 C:Genetics:
 A:Gene: trpE
 C:superfamily: anthranilate synthase component I

Query Match 2.3%; Score 9; DB 2; Length 433;
 Best Local Similarity 100.0%; Pred. No. 0.76;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADS 370
 |||||||||
 Db 401 AGAGIVADS 409

RESULT 9
 A:75163
 anthranilate synthase component I (trpE) PAB2045 - *Pyrococcus abyssi* (strain Orsay)
 C:Species: *Pyrococcus abyssi*
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C:Accession: A75163
 R:Anonymous, Genoscope
 A:Submitted to the EMBL Data Library, July 1999
 A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome stru
 A:Reference number: A75001
 A:Accession: A75163
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-434 <RAM>
 A:Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB49384.1; PID:g545789
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: PAB2045
 C:superfamily: anthranilate synthase component I

Query Match 2.3%; Score 9; DB 2; Length 434;
 Best Local Similarity 100.0%; Pred. No. 0.76;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADS 370
 |||||||||
 Db 402 AGAGIVADS 410

RESULT 10
 A:503316
 anthranilate synthase (EC 4.1.3.27) component I - *Thermus aquaticus*
 C:Species: *Thermus aquaticus*
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 22-Jun-1999
 C:Accession: S03316
 R:Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.
 Biochim. Biophys. Acta 950, 303-312, 1988
 A:Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8 trpE and
 A:Reference number: S03315; MUID:89000781
 A:Accession: S03316
 A:Molecule type: DNA
 A:Residues: 1-462 <SAT>
 A:Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30566.1; PID:g48263
 A:Note: the source is designated as *Thermus thermophilus* HB8
 A:Note: part of this sequence, including the amino end, was confirmed by protein sequend

C:Genetics:
 A:Gene: trpE
 C:Superfamily: anthranilate synthase component I
 C:Keywords: carbon-carbon lyase; oxo-acid-lyase
 F:1-462/Product: anthranilate synthase component I #status experimental <MAT>

Query Match 2.3%; Score 9; DB 2; Length 462;
 Best Local Similarity 100.0%; Pred. No. 0.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADS 370
 |||||||||
 Db 427 AGAGIVADS 435

RESULT 11
 A:69657
 Probable isochorismate synthase (EC 5.4.99.6) menaquinone-specific menF - *Bacillus su*
 C:Species: *Bacillus subtilis*
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: A69657; S27507; S27508; I39883; T46638; T46639
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Bert
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 A.; Ehrlich, S.D.; Emmerson, P.T.; Eutian, K.D.; Erlington, J.; Fabel, C.; Ferrari,
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gall
 tech, J.; Hartwood, C.R.; Henault, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
 Koeltz, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
 Y., M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
 A:Authors: Schleich, S.; Schroeter, R.; Scofield, F.; Seliguchi, J.; Sekowska, A.; Se
 akuch, M.; Tamakoshi, A.; Tanaka, T.; Tempstra, P.; Tognoni, A.; Tosato, V.; Uchiya
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*
 A:Reference number: A69580; MUID:9804033
 A:Accession: A69657
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-471 <KUN>
 A:Cross-references: GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB15061.1; PID:g263555
 A:Experimental source: strain 168
 R:Rowland, B.; Hill, K.; Mueller, J.; Driscoll, J.; Taber, H.
 A:Submitted to the EMBL Data Library, October 1991
 A:Description: Organization of an operon involved in menaquinone biosynthesis in *Baci*
 A:Reference number: S27507
 A:Accession: S27507
 A:Molecule type: DNA
 A:Residues: 1-11, 'K', 13-110, 'MDLCSEDFPLTAKKEVHNGTISKIGSLRLC' <ROW1>
 A:Cross-references: EMBL:M74538; NID:g1185287
 A:Accession: S27508
 A:Molecule type: DNA
 A:Residues: 151-471 <ROW2>
 A:Cross-references: EMBL:M74538; NID:g1185287
 R:Miller, P.
 J. Bacteriol. 170, 2742-2748, 1988
 A:Title: Transcriptional regulation of a promoter in the men gene cluster of *Bacillus*
 A:Reference number: I39883; MUID:88227858
 A:Accession: I39883
 A:Status: translated from GB/EMBL/DDJ
 A:Molecule type: DNA
 A:Residues: 1-11, 'K', 13-32 <MTL>
 A:Cross-references: GB:M21220; NID:g143178; PIDN:AAA22594.1; PID:g551715
 R:Driscoll, J.R.; Taber, H.W.
 J. Bacteriol. 174, 5063-5071, 1992
 A:Title: Sequence organization and regulation of the *Bacillus subtilis* menBE operon.
 A:Reference number: A42715; MUID:92332443
 A:Accession: T46638
 A:Status: preliminary; translated from GB/EMBL/DDJ
 A:Molecule type: DNA
 A:Residues: 1-11, 'K', 13-110, 134-135, 'LCYSE', 141-142, 'LL', 'T', 317, 'AKKEVHN', 325, 'T', 32

A:Cross-references: EMBL:W74521; NID:g557486; PIDN:AAA50396.1; PID:g557487
A:Accession: T46639
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 151-471 <DR2>
A:Cross-references: EMBL:W74521; NID:g557486; PIDN:AAA50397.1; PID:g557488
C:Genetics:
A:Gene: menF
C:Superfamily: isochorismate synthase
C:Keywords: intramolecular transferase; isomerase

Query Match 2.3%: Score 9; DB 1; Length 471;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 LHPYPALGG 306
|||||
Db 376 LHPYPALGG 384

RESULT 12
S75655
anthranilate synthase (EC 4.1.3.27) component I - *Synechocystis* sp. (strain PCC 6803)
N:Alternate names: protein slt1979
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S75655
R:Kaneh, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shingo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* s.
A:Reference number: S74322; MUID:97061201
A:Accession: S75655
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-485 <KAN>
A:Cross-references: EMBL:D90912; GB:AB001339; NID:g1653228; PIDN:BA18216.1; PID:g165330
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: trpE
A:Start codon: GTG
C:Superfamily: anthranilate synthase component I
C:Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match 2.3%: Score 9; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 GAGIVADSD 371
|||||
Db 455 GAGIVADSD 463

RESULT 13
E70352
anthranilate synthase component I - *Aquifex aeolicus*
C:Species: *Aquifex aeolicus*
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 22-Jun-1999
C:Accession: E70352
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
A:Reference number: A70300; MUID:98196666
A:Accession: E70352
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-494 <ROF>
A:Cross-references: GB:AE000656; NID:g2983196; PIDN:AAC06796.1; PID:g2983197; GB:AE00065

A:Experimental source: strain VF5
C:Genetics:
A:Gene: trpE
C:Superfamily: anthranilate synthase component I

Query Match 2.3%: Score 9; DB 2; Length 494;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
|||||
Db 457 AGAGIVADS 465

RESULT 14
JX0065
anthranilate synthase (EC 4.1.3.27) component I - *Clostridium thermocellum*
C:Species: *Clostridium thermocellum*
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Jun-2000
C:Accession: JX0065
R:Sato, S.; Nakada, Y.; Hon-nami, K.; Yasui, K.; Shiratsuchi, A.
J. Biochem. 105, 362-366, 1989
A:Title: Molecular cloning and the nucleotide sequence of the *Clostridium thermocellum*
A:Reference number: JX0065; MUID:89278056
A:Accession: JX0065
A:Molecule type: DNA
A:Residues: 1-494 <SAT>
A:Cross-references: GB:D00399; NID:g216420; PIDN:BA00300.1; PID:g216421
C:Genetics:
A:Gene: trpE
C:Superfamily: anthranilate synthase component I
C:Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match 2.3%: Score 9; DB 2; Length 494;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
|||||
Db 459 AGAGIVADS 467

RESULT 15
C83857
anthranilate synthase trpE [imported] - *Bacillus halodurans* (strain C-125)
C:Species: *Bacillus halodurans*
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
C:Accession: C83857
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* a
A:Reference number: AB3650; MUID:20263314
A:Accession: C83857
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-502 <STO>
A:Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BA05378.1; GSPDB:G
C:Genetics:
A:Gene: trpE
C:Superfamily: anthranilate synthase component I

Query Match 2.3%: Score 9; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
|||||
Db 458 AGAGIVADS 466

Thu Mar 28 13:30:11 2002

us-08-774-104a-2.oli.rpr

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Search completed: March 27, 2002, 15:40:00
Job time: 316 sec

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OM protein - protein search, using sw model

Run on: March 27, 2002, 15:39:39 ; Search time 13.3 seconds
(without alignments)
1094.431 Million cell updates/sec

Title: US-08-774-104a-2

Perfect score: 397
Sequence: 1 MMTYHETRALAQSGLQQLYA.....ETGLKPEPMQLLDYNNHVE 397

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size : 8

Total number of hits satisfying chosen parameters: 21

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	2.5	511	1	TRPE_STRCO
2	10	2.5	523	1	TRPE_HALVO
3	9	2.3	396	1	AMO_AERHY
4	9	2.3	411	1	TRPE_ARCFU
5	9	2.3	433	1	TRPE_PYRKO
6	9	2.3	462	1	TRPE_THETH
7	9	2.3	471	1	MEME_BACSU
8	9	2.3	485	1	TRPE_SYNY3
9	9	2.3	494	1	TRPE_AQUAE
10	9	2.3	494	1	TRPE_CLOTM
11	9	2.3	508	1	TRPE_BACCA
12	9	2.3	508	1	TRPE_BACST
13	9	2.3	508	1	TRPE_SYNY3
14	9	2.3	513	1	TRPE_BACPU
15	9	2.3	515	1	TRPE_BACSU
16	9	2.3	621	1	TRPX_ARATH
17	8	2.0	391	1	ENTC_ECOLI
18	8	2.0	395	1	VIBC_VIBCH
19	8	2.0	403	1	AAT4_ARATH
20	8	2.0	430	1	MEME_HAEIN
21	8	2.0	474	1	TRPE_METJA

ALIGNMENTS

RESULT 1
TRPE_STRCO STANDARD; PRT; 511 AA.
AC Q924W7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
GN TRPE OR SCE8.07C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Saunders D., Harris D., Bentley S.D., Parkhill J., Barrell B.G.,
RA Rajandream M.A.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +
CC PYRUVATE + L-GLUTAMATE.
CC -1- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -1- SUBUNIT: Tetramer of two components I and two components II (by
CC SIMILARITY).
CC -1- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC FAMILY.
CC -----
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CC -----
CC EMBL: AL035654; CAB38585.1;
CC DR InterPro: IPR000350; Chorismate_bind.
CC DR Pfam: PF00425; Chorismate_bind; 1.
CC DR PRINTS: PR00095; ANTSYNTHASE1.
CC DR ProDom: PD000779; Chorismate_bind; 1.
CC KM Tryptophan biosynthesis; Lyase.
CC FT DOMAIN 40
CC SO SEQUENCE 511 AA; 54828 MW; FA3265656CA4DA88 CRC64;

Query Match 2.5%; Score 10; DB 1; Length 511;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 362 AGAGIVADSD 371
DB 476 AGAGIVADSD 485
RESULT 2
TRPE_HALVO STANDARD; PRT; 523 AA.
AC P33975;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
GN TRPE.
OS Halobacterium volcanii (Haloflex volcanii).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloflex.
OX NCBI_TaxID=2246;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MED11;
RC MEDLINE=92165748; Pubmed=1537810;
RA Lam W.L., Logan S.M., Doolittle W.F.;
RT "Genes for tryptophan biosynthesis in the halophilic archaeobacterium
RT Haloflex volcanii: the trpDEG cluster."
RL J. Bacteriol. 174:1694-1697(1992).
CC -1- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +
CC PYRUVATE + L-GLUTAMATE.
CC -1- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.

CC -1- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY
CC SIMILARITY).
CC -1- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC USING AMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC FAMILY.
CC -----
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CC -----
DR EMBL: M83788; AAA73177.1; -.
DR PIR: A42301; A42301.
DR InterPro: IPR000350; Chorismate_bind.
DR Pfam: PF00425; Chorismate_bind; 1.
DR PRINTS: PR00095; ANTSNTHASE1.
DR ProDom: PD000779; Chorismate_bind; 1.
KM Tryptophan biosynthesis: Lyase.
SO SEQUENCE 523 AA; 55920 MW; 9765667997636AC CRC64;

Query Match 2.5%; Score 10; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADSD 371
DB 483 AGAGIVADSD 492

RESULT 3
AMOA_AERHY STANDARD; PRT; 396 AA.
ID AMOA_AERHY
AC P23300;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PUTATIVE ISOCHORISMATE SYNTHASE (EC 5.4.99.6) (AMONABACTIN).
GN AMOA.
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
OC Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=495A2;
RX MEDLINE=91317731; Pubmed=1830579;
RA Bergouhul S., Payne S.M., Arceneaux J.E., Byers B.R.;
RT "Cloning, mutagenesis, and nucleotide sequence of a siderophore
RT biosynthetic gene (amoa) from Aeromonas hydrophila."
RL J. Bacteriol. 173:5121-5128(1991).
CC -1- CATALYTIC ACTIVITY: CHORISMATE - ISOCHORISMATE.
CC -1- PATHWAY: AMONABACTIN BIOSYNTHESIS. AMONABACTIN IS AN IRON-
CC CHELATING COMPOUND INVOLVED IN TRANSPORTING IRON FROM THE
CC BACTERIAL ENVIRONMENT INTO THE CELL CYTOPLASM.
CC -1- SIMILARITY: STRONG. TO OTHER ISOCHORISMATE SYNTHASES: WEAK. TO
CC TRPE AND PAB. B.
CC -----
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CC -----
DR EMBL: M63339; AAA21935.1; -.
DR PIR: A40365; A40365.

DR InterPro: IPR000350; Chorismate_bind.
DR Pfam: PF00425; Chorismate_bind; 1.
DR ProDom: PD000779; Chorismate_bind; 1.
KM Isomerase; Iron transport.
SO SEQUENCE 396 AA; 42074 MW; 5361F4C18EFAAE9D CRC64;

Query Match 2.3%; Score 9; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 360 LFAGAGIVA 368
DB 358 LFAGAGIVA 366

RESULT 4
TRPE_ARCFU STANDARD; PRT; 411 AA.
ID TRPE_ARCFU
AC O28669;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
GN TRPE OR AF1603.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; Pubmed=9389475;
RA Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gilm M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kierlavage A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,
RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -1- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE - ANTHRANILATE +
CC PYRUVATE + L-GLUTAMATE.
CC -1- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -1- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY
CC SIMILARITY).
CC -1- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC USING AMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC FAMILY.
CC -----
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CC -----
DR EMBL: AE000992; AAB89646.1; -.
DR TIGR: AF1603; -.
DR InterPro: IPR000350; Chorismate_bind.
DR Pfam: PF00425; Chorismate_bind; 1.
DR PRINTS: PR00095; ANTSNTHASE1.
DR ProDom: PD000779; Chorismate_bind; 1.
KM Tryptophan biosynthesis: Lyase; Complete proteome.

SQ SEQUENCE 411 AA; 46346 MW; 2D65F91E5BF4457A CRC64;

Query Match 2.3%; Score 9; DB 1; Length 411;

Best Local Similarity 100.0%; Pred. No. 0.31;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADS 370
 |||||||
 DB 381 AGAGIVADS 389

RESULT 5

ID TRPE PYRKO STANDARD; PRT; 433 AA.

AC 09YGB3;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).

GN TRPE.

OS Pyrococcus kodakaraensis.

OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Thermococcus.

OX NCBI_TaxID=69014;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-KOD1;

RX MEDLINE=20092487; PubMed=10628865;

RA Tang X., Ezaki S., Fujiwara S., Takagi M., Imanaka T.;

RT "The tryptophan biosynthesis gene cluster trpCDGFBFA from Pyrococcus

RT kodakaraensis KOD1 is regulated at the transcriptional level and

RT expressed as a single mRNA.";

RL Mol. Genet. 262:815-821(1999).

CC -I- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +

CC PYRUVATE + L-GLUTAMATE.

CC -I- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.

CC -I- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY

CC SIMILARITY).

CC -I- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE

CC USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES

CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.

CC -I- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I

CC FAMILY.

CC -----

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CC -----

CC EMBL: AB030011; BAA82547.1; -;

DR InterPro: IPR000350; Chorismate_bind.

DR Pfam: PF00425; chorismate_bind; 1.

DR PRINTS: PR00095; ANTSMTTHASEI.

DR ProDom: PD000779; Chorismate_bind; 1.

KW Tryptophan biosynthesis; Lyase.

SQ SEQUENCE 433 AA; 48341 MW; E2C539B23365D599 CRC64;

Query Match 2.3%; Score 9; DB 1; Length 433;

Best Local Similarity 100.0%; Pred. No. 0.32;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADS 370
 |||||||
 DB 401 AGAGIVADS 409

RESULT 6

ID TRPE THETH STANDARD; PRT; 462 AA.

AC P05378;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).

GN TRPE.

OS Thermus aquaticus (subsp. thermophilus).

OC Bacteria; Thermus/Delnococcus group; Thermus group; Thermus.

OX NCBI_TaxID=274;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN-HB8 / ATCC 27634;

RX MEDLINE=89000781; PubMed=2844259;

RA Sato S., Nakada Y., Kanaya S., Tanaka T.;

RT "Molecular cloning and nucleotide sequence of Thermus thermophilus

RT HB8 trpE and trpG.";

RL Biochim. Biophys. Acta 950:303-312(1988).

CC -I- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +

CC PYRUVATE + L-GLUTAMATE.

CC -I- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.

CC -I- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY

CC SIMILARITY).

CC -I- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE

CC USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES

CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.

CC -----

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CC -----

CC EMBL: X07744; CAA30566.1; -;

DR PIR: S03316; S03316.

DR InterPro: IPR000350; Chorismate_bind.

DR Pfam: PF00425; chorismate_bind; 1.

DR PRINTS: PR00095; ANTSMTTHASEI.

DR ProDom: PD000779; Chorismate_bind; 1.

KW Tryptophan biosynthesis; Lyase.

SQ SEQUENCE 462 AA; 51635 MW; 62C9AF94B65D010C CRC64;

Query Match 2.3%; Score 9; DB 1; Length 462;

Best Local Similarity 100.0%; Pred. No. 0.34;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADS 370
 |||||||
 DB 427 AGAGIVADS 435

RESULT 7

ID MENF BACSU STANDARD; PRT; 471 AA.

AC P23973; P23972;

DT 01-MAR-1992 (Rel. 21, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE MENAQUINONE-SPECIFIC ISOCHORISMATE SYNTHASE (EC 5.4.99.6).

GN MENF OR ICMS.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Bacillus.

OX NCBI_TaxID=1423;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=168 / RBL;

RX MEDLINE=96144257; PubMed=8566759;

RA Rowland B., Hill K., Miller P., Driscoll J.R., Taber H.W.;

RT "Structural organization of a Bacillus subtilis operon encoding

RT menaquinone biosynthetic enzymes.";

```

RN Gene 167:105-109(1995).
RP SEQUENCE FROM N.A.
RX MEDLINE=98048467; PubMed=9387221;
RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
RT "Sequencing and functional annotation of the Bacillus subtilis genes
   in the 200 kb trnB-dnaB region.";
RL Microbiology 143:3431-3441(1997).
RN (3)
RP PRELIMINARY SEQUENCE FROM N.A.
RC STRAIN=168 / RBL;
RX MEDLINE=92332443; PubMed=1629163;
RA Driscoll J.R., Taber H.W.;
RT "Sequence organization and regulation of the Bacillus subtilis menBE
   operon.";
RL J. Bacteriol. 174:5063-5071(1992).
RN (4)
RP SEQUENCE OF 1-32 FROM N.A.
RX MEDLINE=88227858; PubMed=3131310;
RA Miller P., Mueller J., Hill K., Taber H.W.;
RT "Transcriptional regulation of a promoter in the men gene cluster of
   Bacillus subtilis.";
RL J. Bacteriol. 170:2742-2748(1988).
CC -1- CATALYTIC ACTIVITY: CHORISMATE - ISOCHORISMATE.
CC -1- PATHWAY: MENADIENONE BIOSYNTHESIS.
CC -1- SIMILARITY: STRONG, TO OTHER ISOCHORISMATE SYNTHASES; WEAK, TO
   TRPE AND PABP.
CC -1- CAUTION: USED TO INCLUDE WHAT WAS CALLED 'MEMR'.
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CC -----
DR EMBL: M74538; AAC37013.1; -.
DR EMBL: AF008820; AAC00223.1; -.
DR EMBL: M74521; AAA50396.1; ALT_SEQ.
DR EMBL: M74521; AAA50397.1; ALT_SEQ.
DR EMBL: M21320; AAA22594.1; -.
DR EMBL: Z89119; CAB15061.1; -.
DR PIR: S27508; S27508.
DR PIR: S27507; S27507.
DR Subtilist; BG10682; menF.
DR InterPro: IPR000350; Chorismate_bind.
DR Pfam: PF00425; Chorismate_bind.1.
DR ProDom; PD000779; Chorismate_bind.1.
DR Menaquinone biosynthesis; Isomerase; Complete proteome.
KW CONFLICT 12 E -> K (IN REF. 4).
FT SEQUENCE 471 AA; 52811 MW; 94C047C549FC4CF9 CRC64;
SQ

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Query Match      2.3%; Score 9; DB 1; Length 471;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 298 LHPTPALG 306
   |||||
DB 376 LHPTPALG 384

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RESULT 8
TRPE_SYNY3
ID TRPE_SYNY3 STANDARD; PRT; 485 AA.
AC P74130;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANTHRANILATE SYNTHASE COMPONENT I-LIKE PROTEIN (EC 4.1.3.27).
GN TRPE2 OR SRI1979.
OS Synechocystis sp. (strain PCC 6803).

```

```

OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
ON NCBI_TaxID=1148;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Mureki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
   Synechocystis sp. strain PCC6803. II. Sequence determination of the
   entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE - ANTHRANILATE +
   PYRUVATE + L-GLUTAMATE.
CC -1- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -1- SUBUNIT: Tetramer of two components I and two components II (by
   similarity).
CC -1- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
   USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
   GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
   FAMILY.
CC -1- CAUTION: THIS IS A DIVERGENT FORM OF TRPE. IT IS NOT OBVIOUS IF IT
   IS ACTIVE IN TRP BIOSYNTHESIS.
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CC -----
DR EMBL: D90912; BAA18216.1; -.
DR InterPro: IPR000350; Chorismate_bind.
DR Pfam: PF00425; Chorismate_bind.1.
DR PRINTS: PR00095; ANTSYNTHASE1.
DR ProDom; PD000779; Chorismate_bind.1.
KW Tryptophan biosynthesis; Lyase; Complete proteome.
SQ SEQUENCE 485 AA; 54270 MW; 4F25ECB3897BC7C CRC64;

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Query Match      2.3%; Score 9; DB 1; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 363 GAGIVADSD 371
   |||||
DB 455 GAGIVADSD 463

```

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RESULT 9
TRPE_AQUAE
ID TRPE_AQUAE STANDARD; PRT; 494 AA.
AC 066849;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
GN TRPE OR AQ_582.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VP5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex

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RF .aeolicus."
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +
CC PYRUVATE + L-GLUTAMATE.
CC -1- SUBUNIT: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -1- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY
CC SIMILARITY).
CC -1- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC FAMILY.
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CC -----
CC EMBL: AE000696; AAC06796.1; -.
CC InterPro: IPR000350; Chorismate_bind.
CC Pfam: PF00425; chorismate_bind; 1.
CC PRINTS: PR000095; ANTSNTHASEI.
CC ProDom: PD000779; Chorismate_bind; 1.
CC TrpTropPhan biosynthesis; Lyase; Complete proteome.
CC SEQUENCE 494 AA; 57087 MW; AC20BBB260867CEC CRC64;

```

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Query Match      2.3%; Score 9; DB 1; Length 494;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 362 AGAGIVADS 370
   |||||
DB 457 AGAGIVADS 465

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RESULT 10
TRPE_CLOTM STANDARD; PRT; 494 AA.
ID TRPE_CLOTM STANDARD; PRT; 494 AA.
AC P14953;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
GN TRPE.
OS Clostridium thermocellum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_Taxid=1515;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89278056; PubMed=2732211;
RA Sato S., Nakada Y., Hon-Nami K., Yasui K., Shiratsuchi A.;
RT "Molecular cloning and the nucleotide sequence of the Clostridium
RT thermocellum trpe gene."
RL J. Biochem. 105:362-366(1989).
CC -1- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +
CC PYRUVATE + L-GLUTAMATE.
CC -1- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -1- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY
CC SIMILARITY).
CC -1- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D00399; BAA00300.1; -.
CC PIR: JX0065; JX0065.
CC InterPro: IPR000350; Chorismate_bind.
CC Pfam: PF00425; chorismate_bind; 1.
CC PRINTS: PR000095; ANTSNTHASEI.
CC ProDom: PD000779; Chorismate_bind; 1.
CC TrpTropPhan biosynthesis; Lyase.
CC SEQUENCE 494 AA; 56020 MW; 32DF1EF22344447D CRC64;

```

```

Query Match      2.3%; Score 9; DB 1; Length 494;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 362 AGAGIVADS 370
   |||||
DB 459 AGAGIVADS 467

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RESULT 11
TRPE_BACCA STANDARD; PRT; 508 AA.
ID TRPE_BACCA STANDARD; PRT; 508 AA.
AC P30526;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
GN TRPE.
OS Bacillus caldotenax.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_Taxid=1395;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92062737; PubMed=1840498;
RA Shiratsuchi A., Sato S.;
RT "Nucleotide sequence of trpe, anthranilate synthase I gene, of
RT Bacillus caldotenax."
RL Biochim. Biophys. Acta 1090:348-350(1991).
CC -1- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +
CC PYRUVATE + L-GLUTAMATE.
CC -1- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -1- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY
CC SIMILARITY).
CC -1- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC FAMILY.
CC -----
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CC -----
CC EMBL: X55703; CAA39230.1; -.
CC PIR: S21416; S21416.
CC PIR: S19266; S19266.
CC InterPro: IPR000350; Chorismate_bind.
CC Pfam: PF00425; chorismate_bind; 1.
CC PRINTS: PR000095; ANTSNTHASEI.
CC ProDom: PD000779; Chorismate_bind; 1.
CC TrpTropPhan biosynthesis; Lyase.
CC SEQUENCE 508 AA; 56492 MW; 3DA1130811A77797 CRC64;

```

Query Match 2.3%; Score 9; DB 1; Length 508;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
|||||
Db 465 AGAGIVADS 473

RESULT 12

TRPE_BACST STANDARD; PRT; 508 AA.
AC Q9X604;
AD 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
GN ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12980 / NCA 26;
RX MEDLINE=99299394; PubMed=10369778;
RA Chen X.-P., Atkinson A.A., Yang M., Baumann C., Dodson E.J.,
RA Dodson G.G., Gollnick P.;
RT "Regulatory features of the trp operon and the crystal structure of
RT the trp RNA-binding attenuation protein from Bacillus
RT stearothermophilus.";
RL J. Mol. Biol. 289:1003-1016(1999).
CC -I- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +
CC PYRUVATE + L-GLUTAMATE.
CC -I- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -I- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY
CC SIMILARITY).
CC -I- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -I- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL: AF139534; AAD33791.1; -;
DR InterPro: IPR000350; Chorismate_bind.
DR Pfam: PF00425; Chorismate_bind; 1.
DR PRINTS: PR00095; ANTSNTNASEI.
DR ProDom: PD000779; Chorismate_bind; 1.
KW Tryptophan biosynthesis; Lyase.
SQ SEQUENCE 508 AA; 56440 MW; 25EB252616160ADD CRC64;

Query Match 2.3%; Score 9; DB 1; Length 508;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
|||||
Db 465 AGAGIVADS 473

RESULT 13
TRPE_SYNT3 STANDARD; PRT; 508 AA.

AC P20170; P20168;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROBABLE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
GN TRPE OR SLR0738.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nairu K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
RN [2]

RP SEQUENCE OF 1-408 FROM N.A.
RX MEDLINE=89034300; PubMed=3141423;
RA Reilly P., Humes J.D., Pan Y.C.E., Nelson N.;
RT "Molecular cloning and sequencing of the psad gene encoding subunit
RT II of photosystem I from the cyanobacterium, Synechocystis sp. PCC
RT 6803.";
RL J. Biol. Chem. 263:17658-17662(1988).

CC -I- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +
CC PYRUVATE + L-GLUTAMATE.
CC -I- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -I- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY
CC SIMILARITY).
CC -I- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -I- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC FAMILY.
CC -I- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 182.

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CC EMBL: D90899; BAA16689.1; -;
DR EMBL: J04195; AAA88626.1; ALT_FRAME.
DR EMBL: J04195; AAA88627.1; ALT_FRAME.
DR PIR: B32124; B32124.
DR PIR: C32124; C32124.
DR InterPro: IPR000350; Chorismate_bind.
DR Pfam: PF00425; Chorismate_bind; 1.
DR PRINTS: PR00095; ANTSNTNASEI.
DR ProDom: PD000779; Chorismate_bind; 1.
KW Tryptophan biosynthesis; Lyase; Complete proteome.
SQ SEQUENCE 508 AA; 57147 MW; A3308E9A7B8A1FC1 CRC64;

Query Match 2.3%; Score 9; DB 1; Length 508;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 GAGIVADSD 371
|||||
Db 477 GAGIVADSD 485

RESULT 14

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TRPE_BACPU          STANDARD:      PRT:      513 AA.
ID   TRPE_BACPU          STANDARD:      PRT:      513 AA.
AC   P18267;
DT   01-NOV-1990 (Rel. 16, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
GN   TRPE.
OS   Bacillus pumilus (Bacillus mesentericus).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Bacillus.
OX   NCBI_TaxID=1408;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN-RUB502;
RX   MEDLINE=90236301; PubMed=2110100;
RA   Rivas M.V., Jarvis E.D., Rudner R.;
RT   "The structure of the trpe, trpd and 5' trpc genes of Bacillus
RT   pumilus."
RL   Gene 87:71-78(1990).
RN   [2]
RP   ERRATUM
RX   MEDLINE=91033058; PubMed=2227447;
RA   Rivas M.V., Jarvis E.D., Rudner R.;
RL   Gene 94:141-143(1990).
CC   -1- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +
CC   PYRUVATE + L-GLUTAMATE.
CC   -1- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC   -1- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY
CC   SIMILARITY).
CC   -1- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC   USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC   GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC   -1- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC   FAMILY.
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CC   -----
DR   EMBL: M36468; AAB02272.1; ALT_INIT.
DR   PIR: JH0098; JH0098.
DR   InterPro: IPR000350; Chorisimate_bind.
DR   Pfam: PF00425; Chorisimate_bind; 1.
DR   ProDom: PD000779; Chorisimate_bind; 1.
DR   TrpTophan biosynthesis; Lyase.
SQ   SEQUENCE 513 AA; 58091 MW; 0E6B19904421CC5A CRC64;

Query Match          2.3%; Score 9; DB 1; Length 513;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
DB 462 AGAGIVADS 470

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OC   Bacillus/Staphylococcus group; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Henner D.J.;
RT   "Sequence of Bacillus subtilis dbpA, mtr(A,B), gerc(1-3), ndk, cher,
RT   aro(B,E,F,H), trp(A-F), hisH, and tyra genes."
RL   Submitted (JAN-1992) to the EMBL/GenBank/DBD databases.
RN   [2]
RP   PRELIMINARY SEQUENCE FROM N.A.
RC   MEDLINE=85232062; PubMed=3924737;
RA   Henner D.J., Band L., Shimotsu H.;
RT   "Nucleotide sequence of the Bacillus subtilis tryptophan operon."
RL   Gene 34:169-177(1985).
RN   [3]
RP   PRELIMINARY SEQUENCE FROM N.A.
RC   MEDLINE=84183611; PubMed=6425119;
RA   Band L., Shimotsu H., Henner D.J.;
RT   "Nucleotide sequence of the Bacillus subtilis trpe and trpd genes."
RL   Gene 27:55-65(1984).
RN   [4]
RP   SEQUENCE OF 1-40 FROM N.A.
RX   MEDLINE=85038507; PubMed=6436812;
RA   Shimotsu H., Henner D.J.;
RT   "Characterization of the Bacillus subtilis tryptophan promoter
RT   region."
RL   Proc. Natl. Acad. Sci. U.S.A. 81:6315-6319(1984).
CC   -1- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +
CC   PYRUVATE + L-GLUTAMATE.
CC   -1- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC   -1- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY
CC   SIMILARITY).
CC   -1- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC   USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC   GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC   -1- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC   FAMILY.
CC   -1- CAUTION: REF.2 AND REF.3 SEQUENCES DIFFER FROM THAT SHOWN IN
CC   POSITIONS 343 TO 402 DUE TO A FRAMESHIFT.
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CC   -----
DR   EMBL: M80245; AAA20862.1; -.
DR   EMBL: K01391; AAA22865.1; -.
DR   EMBL: M27566; AAA22875.1; -.
DR   EMBL: Z99115; CAB14184.1; -.
DR   PIR: A01119; NNEB1.
DR   PIR: A22063; A22063.
DR   PIR: A22794; A22794.
DR   Subtilist; BG10287; trpe.
DR   InterPro: IPR000350; Chorisimate_bind.
DR   Pfam: PF00425; Chorisimate_bind; 1.
DR   PRINTS: PR00095; ANTSNTHTASE1.
DR   ProDom: PD000779; Chorisimate_bind; 1.
DR   TrpTophan biosynthesis; Lyase; Complete proteome.
KW   CONFLICT 80 A -> P (IN REF. 2 AND 3).
FT   CONFLICT 120 80 A -> S (IN REF. 2 AND 3).
SQ   SEQUENCE 515 AA; 58116 MW; 33B8BD9D80BCD991 CRC64;

Query Match          2.3%; Score 9; DB 1; Length 515;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
DB 464 AGAGIVADS 472

```

Search completed: March 27, 2002, 15:43:04
Job time: 205 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 27, 2002, 15:39:09 ; Search time 25.43 Seconds
(without alignments)
2283.528 Million cell updates/sec

Title: US-08-774-104A-2
Perfect score: 397
Sequence: 1 MMTYHETRALAQSDLDQLVA.....ETGLKFEPRMRLKDYNHVE 397

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 473505 seqs, 146272329 residues

Word size : 8

Total number of hits satisfying chosen parameters: 22

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: SPREMBL_17.*
2: sp_archaea.*
3: sp_bacteria.*
4: sp_fungi.*
5: sp_human.*
6: sp_invertebrate.*
7: sp_mammal.*
8: sp_mhc.*
9: sp_organelle.*
10: sp_plant.*
11: sp_fodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	339	85.4	398	4 Q9UIA3	Q9uia3 homo sapien
2	10	2.5	524	2 O9A490	O9a490 caulobacter
3	10	2.5	526	10 O9LY58	O9ly58 arabidopsis
4	10	2.5	608	10 Q41155	Q41155 rula graveo
5	10	2.5	608	10 O9AW95	O9aw95 catharanthu
6	10	2.5	613	10 Q41156	Q41156 rula graveo
7	9	2.3	404	2 O9CHJ9	O9chj9 lactococcus
8	9	2.3	434	1 O9Y1G5	O9y1g5 pyrococcus
9	9	2.3	453	2 O99V51	O99v51 staphylococ
10	9	2.3	502	2 O9KCB4	O9kcb4 bacillus ha
11	9	2.3	577	10 O9XJ30	O9xj30 oryza sativ
12	9	2.3	606	10 O9XJ29	O9xj29 oryza sativ
13	8	2.0	141	2 O9A1P3	O9a1p3 streptococc
14	8	2.0	141	2 O9I166	O9i166 pseudomonas
15	8	2.0	387	10 O9S169	O9s169 arabidopsis
16	8	2.0	391	2 P93475	P93475 pseudomonas
17	8	2.0	408	2 O9F639	O9f639 stigmatella
18	8	2.0	427	2 O9E280	O9e280 bruceella ab
19	8	2.0	436	4 O9H8R2	O9h8r2 homo sapien

20 8 2.0 441 2 Q9PBV0 Q9pbv0 xylella fasc
21 8 2.0 616 10 O81533 O81533 nicotiana t
22 8 2.0 1081 6 Q9BE73 Q9be73 macaca fasc

ALIGNMENTS

RESULT 1
ID Q9UIA3 PRELIMINARY: PRT; 398 AA.
AC Q9UIA3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE NEUTRAL SPHINGOMYELINASE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=20069736; PubMed=10601312;
RA Chatterjee S., Han H., Rollins S., Cleveland T.;
RT "Molecular cloning, characterization, and expression of a novel human
RT neutral sphingomyelinase."
RL J. Biol. Chem. 274:37407-37412(1999).
DR EMBL: AF069740; AAF19052.1; -;
DR InterPro: IPR000350; ChorisMate_bind.
DR Pfam: PF00425; ChorisMate_bind; 1.
DR PRINTS: PR00095; ANTSNTHASEI.
DR ProDom: PD000779; ChorisMate_bind; 1.
SQ SEQUENCE 398 AA; 43590 MW; 0248D89974C77BC1 CRC64;

Query Match 85.4%; Score 339; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 59 VFGAQSFEDEQYPOSELMAGFWFVPEVMVTIAADKITFGSDTVSDEFTWLAQFVPRKQNT 118
DB 60 VFGAQSFEDEQYPOSELMAGFWFVPEVMVTIAADKITFGSDTVSDEFTWLAQFVPRKQNT 119
QY 119 VTSHTYDEVDWTERENLIDTIAIDOTLAKVYFGQOTQLSDTLRLAQIITALEQAN 178
DB 120 VTSHTYDEVDWTERENLIDTIAIDOTLAKVYFGQOTQLSDTLRLAQIITALEQAN 179
QY 179 TYHVLKRDHDLFISATPERLVAMSGQITAAVAGTSRGTGAGDIALGEALLASOKN 238
DB 180 TYHVLKRDHDLFISATPERLVAMSGQITAAVAGTSRGTGAGDIALGEALLASOKN 239
QY 239 RIEHQYVASITTRLDVTTSLKVPAMPISLKKQVOHLVPTTGDIHAHLSTAVTAVDRL 298
DB 240 RIEHQYVASITTRLDVTTSLKVPAMPISLKKQVOHLVPTTGDIHAHLSTAVTAVDRL 299
QY 299 HRPRLAGVYPRALYVIAHEKTPRGIPFAGIPGTFADNSGEFVVGIRSMYVNOQRRA 358
DB 300 HRPRLAGVYPRALYVIAHEKTPRGIPFAGIPGTFADNSGEFVVGIRSMYVNOQRRA 359
QY 359 TEFAGAGIVADSDAOOEYETGLKFEPRMRLKDYNHVE 397
DB 360 TEFAGAGIVADSDAOOEYETGLKFEPRMRLKDYNHVE 398
RESULT 2
ID Q9A490 PRELIMINARY: PRT; 524 AA.
AC Q9A490;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE PARA-AMINOBENZATE SYNTHASE, COMPONENT I.

GN CC2953.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Caulobacter.
 OX NCB1_TaxID=69394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21173698; PubMed=11259647;
 RA Nleman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Knouri H., Shetty J., Berry K.,
 RA Ullendack T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL: AE005959; AAK24915.1; -
 DR TIGR: CC2953; -
 KW Complete proteome.
 SQ SEQUENCE 524 AA; 55526 MW; 680D4B427AAAD5D CRC64;

Query Match 2.5%; Score 10; DB 10; Length 524;
 Best Local Similarity 100.0%; Pred. No. 0.26;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADSD 371
 |||||
 DB 494 AGAGIVADSD 503

RESULT 3
 O9LY58 PRELIMINARY; PRT; 526 AA.
 AC O9LY58:
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE ANTHRANILATE SYNTHASE ALPHA-1 CHAIN-LIKE PROTEIN.
 GN F27K19.50.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCB1_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Benes V., Wurmbach E., Drzonek H., Ansoerge W., Mewes H.W., Rudd S.,
 RA Lemcke K., Mayer K.F.X., Quettler F., Salanoubat M.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project:
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL163832; CAB87841.1; -
 DR InterPro: IPR000350; Chorisimate_bind.
 DR Pfam: PF00425; Chorisimate_bind.1.
 DR PRINTS: PR00095; ANTSNTHASEI.
 DR ProDom: PD000779; Chorisimate_bind.1.
 SQ SEQUENCE 526 AA; 59296 MW; AB4D4F4AA73966C CRC64;

Query Match 2.5%; Score 10; DB 10; Length 526;
 Best Local Similarity 100.0%; Pred. No. 0.26;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADSD 371
 |||||
 DB 483 AGAGIVADSD 492

RESULT 4

O41155
 ID Q41155 PRELIMINARY; PRT; 608 AA.
 AC Q41155:
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE ANTHRANILATE SYNTHASE ALPHA SUBUNIT PRECURSOR.
 OS Ruta graveolens (common rue).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Sapindales; Rutaceae; Ruta.
 OX NCB1_TaxID=37565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95276783; PubMed=7757119;
 RA Bohlmann J., Deluca V., Eilert U., Martin W.;
 RT "Purification and cDNA cloning of anthranilate synthase from Ruta
 graveolens: modes of expression and properties of native and
 recombinant enzymes.";
 RL Plant J. 7:491-501(1995).
 DR EMBL: L34343; AAN74900.1; -
 DR HSSP: Q06128; IQDL.
 DR Mendel: 12275; Rutgr:1433;12275.
 DR InterPro: IPR000350; Chorisimate_bind.
 DR Pfam: PF00425; Chorisimate_bind.1.
 DR PRINTS: PR00095; ANTSNTHASEI.
 DR ProDom: PD000779; Chorisimate_bind.1.
 KW Signal.
 FT SIGNAL 1 89 POTENTIAL.
 FT CHAIN 90 608 ANTHRANILATE SYNTHASE ALPHA SUBUNIT.
 SQ SEQUENCE 608 AA; 67992 MW; 40F7DB56FA9366A5 CRC64;

Query Match 2.5%; Score 10; DB 10; Length 608;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADSD 371
 |||||
 DB 570 AGAGIVADSD 579

RESULT 5
 O9AW95 PRELIMINARY; PRT; 608 AA.
 AC O9AW95:
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE ANTHRANILATE SYNTHASE ALPHA SUBUNIT (EC 4.1.3.27).
 GN ASA.
 OS Catharanthus roseus (Rosa periwinkle) (Madagascar periwinkle).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; eusterids I; Gentianales; Apocynaceae; Catharanthus.
 OX NCB1_TaxID=4058;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G.DON; TISSUE=CELL SUSPENSION;
 RA Bongers R.J.M., Meijer A.H., Hoge J.H.C., Verpoorte R.;
 RT "Molecular cloning and characterization of a cDNA clone encoding the
 alpha-subunit of the enzyme anthranilate synthase from Catharanthus
 roseus.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ250008; CAC29060.1; -
 KW lyase.
 SQ SEQUENCE 608 AA; 68263 MW; DE052CE5A1FC15E CRC64;

Query Match 2.5%; Score 10; DB 10; Length 608;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADSD 371
 |||||
 DB 570 AGAGIVADSD 581

RESULT 6
 ID 041156 PRELIMINARY; PRT; 613 AA.
 AC 041156;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ANTHRANILATE SYNTHASE ALPHA SUBUNIT PRECURSOR.
 OS Ruta graveolens (common rue).
 OS Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:
 OC eurosids II: Sapindales: Rutaceae; Ruta.
 OX NCBI_TaxID=37565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9526783; PubMed=7757119;
 RA Bohlmann J., Deluca V., Eilert U., Martin W.
 RT Purification and cDNA cloning of anthranilate synthase from Ruta
 RT graveolens: modes of expression and properties of native and
 RT recombinant enzymes.*;
 RT
 RL Plant J. 7:491-501(1995).
 DR EMBL: L34344; AAA74901.1; -
 DR HSSP: Q06128; 10DL.
 DR Mendel: 12276; Rutgr:143;12276.
 DR InterPro: IPR000350; Chorisimate_bind.
 DR Pfam: PF00425; Chorisimate_bind; 1.
 DR PRINTS: PR00095; ANTSNTHASEI.
 DR ProDom: PD000779; Chorisimate_bind; 1.
 KW Signal.
 KM SIGNAL.
 FT CHAIN 1 92 POTENTIAL.
 FT SIGNAL 93 613 ANTHRANILATE SYNTHASE ALPHA SUBUNIT.
 SQ SEQUENCE 613 AA; 67918 MW; 9986339474ABFF76 CRC64;

Query Match 2.5%; Score 10; DB 10; Length 613;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADSD 371
 |||||
 DB 572 AGAGIVADSD 581

RESULT 7
 ID 09CHJ9 PRELIMINARY; PRT; 404 AA.
 AC 09CHJ9;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE MENAQUINONE-SPECIFIC ISOCHORISMATE SYNTHASE (EC 5.4.99.6).
 GN MENF.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-IL1403;
 RA Bolotin A., Wincker P., Manger S., Jaillon O., Malarne K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis.";
 RL Genome Res. 0:0-0(2001).
 DR EMBL: AE006306; AA04830.1; -
 DR InterPro: IPR000350; Chorisimate_bind.
 DR Pfam: PF00425; Chorisimate_bind; 1.
 DR ProDom: PD000779; Chorisimate_bind; 1.

KW Complete proteome.
 SQ SEQUENCE 404 AA; 46450 MW; 83BFC659F45AB060 CRC64;

Query Match 2.3%; Score 9; DB 2; Length 404;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 298 LHPPALGG 306
 |||||
 DB 314 LHPPALGG 322

RESULT 8
 ID 09V1G5 PRELIMINARY; PRT; 434 AA.
 AC 09V1G5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ANTHRANILATE SYNTHASE COMPONENT I (TRPE).
 GN PAB2045.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 OX NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ORSAY;
 RA Heilig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 RT structure and evolution.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A1248284; CAB49384.1; -
 DR HSSP: Q06128; 10DL.
 DR InterPro: IPR000350; Chorisimate_bind.
 DR Pfam: PF00425; Chorisimate_bind; 1.
 DR PRINTS: PR00095; ANTSNTHASEI.
 DR ProDom: PD000779; Chorisimate_bind; 1.
 KW Complete proteome.
 SQ SEQUENCE 434 AA; 49058 MW; 1FFBF19D48BD193C CRC64;

Query Match 2.3%; Score 9; DB 1; Length 434;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADS 370
 |||||
 DB 402 AGAGIVADS 410

RESULT 9
 ID 099V51 PRELIMINARY; PRT; 453 AA.
 AC 099V51;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SA0895 PROTEIN.
 GN SA0895.
 OS Staphylococcus aureus subsp. aureus N315.
 OC Bacteria: Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Chii I., Oguchi A., Aoki K.I., Nagai Y., Ito T., Kanamori M.,
 RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
 RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
 RA Hiraoka H., Kohara S., Goto S., Yabuuchi J., Kanehisa M.,
 RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shida T., Hattori M.,
 RA Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT aureus."
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003132; BAB42140.1;
 KW Complete proteome.
 SQ SEQUENCE 453 AA; 52245 MW; E0FBD2C9C30B3161 CRC64;

Query Match 2.3%; Score 9; DB 2; Length 453;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 298 LHPPALCG 306
 Db 355 LHPPALCG 363

RESULT 10
 ID O9KCB4 PRELIMINARY; PRT; 502 AA.
 AC O9KCB4;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE ANTHRANILATE SYNTHASE.
 GN TRPE OR BH1659.
 OS *Bacillus halodurans*.
 OC Bacteria; Firmicutes; *Bacillus/Clostridium* group;
 OC *Bacillus/Staphylococcus* group; *Bacillus*.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C-125 / JCM 9153;
 RC MDLINE-20512582; PubMed-11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kohara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus*
 RT *halodurans* and genomic sequence comparison with *Bacillus subtilis*."
 RL EMBL; AP001512; BAB05378.1;
 DR InterPro: IPR000350; ChoriSmate_bind.
 DR Pfam: PF00425; ChoriSmate_bind.1.
 DR PRINTS; PR00095; ANTSYNTHASE1.
 DR ProDom: PD000779; ChoriSmate_bind.1.
 KW Complete proteome.
 SQ SEQUENCE 502 AA; 56349 MW; D844E9AB2689551B CRC64;

Query Match 2.3%; Score 9; DB 2; Length 502;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADS 370
 Db 458 AGAGIVADS 466

RESULT 11
 ID O9XJ30 PRELIMINARY; PRT; 577 AA.
 AC O9XJ30;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE ANTHRANILATE SYNTHASE ALPHA 1 SUBUNIT.
 GN OSAS1.
 OS *Oryza sativa* (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihartoideae; Oryzeae; *Oryza*.
 OX NCBI_TaxID=4530;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-CV. NIPPONBARE;
 RA Tozawa Y., Hasegawa H., Terakawa T., Wakasa K.;
 RT "Rice cDNA encoding anthranilate synthase alpha subunit."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB022602; BAA82094.1;
 DR HSP; 006128; 10DL.
 DR InterPro: IPR000350; ChoriSmate_bind.
 DR Pfam: PF00425; ChoriSmate_bind.1.
 DR PRINTS; PR00095; ANTSYNTHASE1.
 DR ProDom: PD000779; ChoriSmate_bind.1.
 SQ SEQUENCE 577 AA; 63947 MW; D280F8733809AC38 CRC64;

Query Match 2.3%; Score 9; DB 10; Length 577;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADS 370
 Db 539 AGAGIVADS 547

RESULT 12
 ID O9XJ29 PRELIMINARY; PRT; 606 AA.
 AC O9XJ29;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE ANTHRANILATE SYNTHASE ALPHA 2 SUBUNIT.
 GN OSAS2.
 OS *Oryza sativa* (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihartoideae; Oryzeae; *Oryza*.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. NIPPONBARE;
 RA Tozawa Y., Hasegawa H., Terakawa T., Wakasa K.;
 RT "Rice cDNA encoding anthranilate synthase alpha subunit."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB022603; BAA82095.1;
 DR HSP; 006128; 10DL.
 DR InterPro: IPR000350; ChoriSmate_bind.
 DR Pfam: PF00425; ChoriSmate_bind.1.
 DR PRINTS; PR00095; ANTSYNTHASE1.
 DR ProDom: PD000779; ChoriSmate_bind.1.
 DR ProSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
 SQ SEQUENCE 606 AA; 66988 MW; A74AB7CE986F0608 CRC64;

Query Match 2.3%; Score 9; DB 10; Length 606;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADS 370
 Db 567 AGAGIVADS 575

RESULT 13
 ID O9AIP3 PRELIMINARY; PRT; 55 AA.
 AC O9AIP3;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE HYPOTHEICAL PROTEIN SPY0170.
 GN SPY0170.
 OS *Streptococcus pyogenes*.

```

OC Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370;
RA MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL: AE006486; AAK33270.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 55 AA; 5908 MW; B0DEF0F67F137109 CRC64;

Query Match 2.0%; Score 8; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 207 IATAVAG 214
DB 10 IATAVAG 17

RESULT 14
OY 091166 PRELIMINARY; PRT; 141 AA.
AC 091166;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE HYPOTHEICAL PROTEIN PA2415.
GN PA2415.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RA MEDLINE=20437337; PubMed=10984043;
RA Stoyer C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Coltry L., Tolentino E., Westbrook-Wadman S., Yan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL: AE004668; AAG05803.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 141 AA; 15171 MW; D6CC5F8B415421E0 CRC64;

Query Match 2.0%; Score 8; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 227 ALGALLA 234
DB 125 ALGALLA 132

RESULT 15
OY 095169 PRELIMINARY; PRT; 387 AA.
AC 095169;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

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DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE F33N19.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Walker M., Shinn P., Brooks S., Buehler E., Chao Q., Dunn P., Khan S.,
RA Kim C., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A.,
RA Hansen N.F., Hulzar L., Kremetska I., Lenz C., Li J., Liu S.,
RA Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G.,
RA Davis R.W., Federapfel N.A., Theologis A., Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F33N19 from chromosome
RT 1.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
CC -1- SIMILARITY: TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL: AC007190; AAF19543.1;
DR HSSP: P00508; 7AAT.
DR InterPro: IPR001511; Aminotran_1.
DR InterPro: IPR000796; Asp_aminotransfrase.
DR Pfam: PF00155; aminotran_1; 1.
DR PRINTS: PR00799; TRANSAMINASE.
DR PROSITE: PS00105; AA_TRANSFER_CLASS_1; 1.
KW Pyridoxal phosphate.
SQ SEQUENCE 387 AA; 42723 MW; 5857C262340E9E1B CRC64;

Query Match 2.0%; Score 8; DB 10; Length 387;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 QOLYALE 23
DB 337 QOLYALE 344

```

Search completed: March 27, 2002, 15:42:44
 Job time: 215 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 27, 2002, 15:34:44 ; Search time 24.81 seconds
(without alignments)
1185.292 Million cell updates/sec

Title: US-08-774-104A-2

Perfect score: 397
Sequence: 1 MMTYHETRALAQSDLQQLYA.....ETGKFEPMQLKDYNHVE 397

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 8

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

A.Geneseq-1101:*

- 1: /SID58/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SID58/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SID58/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SID58/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SID58/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /SID58/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SID58/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SID58/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SID58/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SID58/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SID58/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SID58/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SID58/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SID58/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /SID58/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /SID58/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	397	100.0	397	19	AAW69162	Human neutral sph
2	397	100.0	397	21	AAW69162	Amino acid sequenc
3	92	2.3	92	20	AAV42118	Wheat anthranilate
4	92	2.3	446	20	AAV42118	Corn anthranilate
5	92	2.3	577	20	AAW93815	Rice ASA first iso
6	92	2.3	577	20	AAW93810	Rice anthranilate
7	92	2.3	603	20	AAV42112	Corn anthranilate
8	92	2.3	606	20	AAW93814	Rice anthranilate
9	92	2.3	615	18	AAW26685	Maize C28 allele a
10	92	2.3	615	18	AAW26686	Maize anthranilate
11	8	2.0	271	20	AAV33698	E. coli entc prote

12	8	2.0	287	21	AAW08519	Protein encoded by
13	8	2.0	313	22	AAW0815	Human bone marrow
14	8	2.0	331	20	AAV50338	P. fluorescens ICS
15	8	2.0	391	20	AAV50335	E. coli entc prote
16	8	2.0	391	20	AAV50336	P. fluorescens ICS
17	8	2.0	427	22	AAW00928	Human bone marrow
18	8	2.0	428	22	AAW00981	Human bone marrow
19	8	2.0	436	22	AAW94564	Human protein sequ
20	8	2.0	616	20	AAV41301	Tobacco anthranilla

ALIGNMENTS

RESULT	1	ALIGNMENTS
AAW69162	standard; Protein; 397 AA.	
ID	AAW69162;	
AC	AAW69162;	
XX	20-OCT-1998 (first entry)	
DT		
XX		
DE	Human neutral sphingomyelinase.	
XX		
KW	Human; neutral sphingomyelinase; N-SMase; diagnosis; Crohn's disease;	
KM	obesity; diabetes; Alzheimer's disease.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 59	/note="encoded by GTCGTT"
XX		
PN	W09828445-A1.	
XX		
PD	02-JUL-1998.	
XX		
PF	23-DEC-1997; 97MO-US24051.	
XX		
PR	24-DEC-1996; 96US-0774104.	
XX		
XX	(UYJO) UNIV JOHNS HOPKINS.	
PA		
XX		
PI	Chatterjee S;	
XX		
DR	WPI; 1998-377673/32.	
XX		
PT	N-PSDB; AAV41196.	
PT	Human neutral sphingomyelinase - used to, e.g. treat N-SMase	
PT	associated disorders, e.g. Crohn's disease, obesity, diabetes, and	
PT	Alzheimer's disease	
XX		
PS	Claim 19; Page 29-30; 47pp; English.	
XX		
XX	The present sequence represents human neutral sphingomyelinase (N-SMase).	
CC	A host cell containing a vector comprising a nucleotide sequence	
CC	encoding N-SMase can be used to produce N-SMase. N-SMase can be used in	
CC	a method for identifying a compound useful in the diagnosis or treatment	
CC	of a human neutral sphingomyelinase related disorder. N-SMase, and a	
CC	nucleotide sequence encoding N-SMase, can be used for modulating N-SMase	
CC	activity, and for treating a disorder associated with N-SMase. The	
CC	N-SMase disorders that can be treated with the nucleotide sequence or	
CC	N-SMase, is an inflammatory disorder, arthritis, osteoarthritis, Crohn's	
CC	disease, obesity, diabetes, cirrhosis, susceptible tumours, central	
CC	nervous system disorder, vascular stenosis, arterial occlusion arising	
CC	from plaque formation, cardiac disease where LV dysfunction occurs,	
CC	hypercholesterolaemia, cholesterol ester storage disorder, renal failure,	
CC	HIV infection, depression, schizophrenia, neurodegeneration, and	
CC	Alzheimer's disease. An antibody against N-SMase can be used to reduce	
CC	tumour necrosis factor alpha (TNF-alpha) induced apoptosis of mammalian	
CC	cells.	
XX	Sequence 397 AA;	

Query Match 100.0%; Score 397; DB 19; Length 397;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTYHETRALAQSDDLQDLVALETTERGAYFAPPADTLRFGIGAITAKTAALOGAVF 60
 |||||||
 Db 1 mmythetralaqsdlqdlvaaleetefgayfapaddtlrfgigataktakagavf 60

QY 61 GAOSFDEQEPSEELMGFVPEVMTIADKTFEGSDIVSDPTTWLAQFVPRQPTVT 120
 |||||||
 Db 61 gagsfdeqepseelmagfvpewmvtiaadkltfsgdsvsdlttwlaqfvpkqptvt 120

QY 121 TSHVTDEVDNIERTENLIDTLAIDQTLAKVVFGRQOTLQSDTLRLAQIIRALAEQANTY 180
 |||||||
 Db 121 tshvtdevdnterentlidlalidqtlakvfvgrqqlqsdltlrlaqiiralaeganty 180

QY 181 HVLKRNDELFIATPRLVAMSGGIATAVAGTSRRGTGADIALGELLASQKNRI 240
 |||||||
 Db 181 hvltkrdelfiatprrlvamsggiataavagtsrrgtgdadialgellalsqknri 240

QY 241 EHQYVVASITTRLODVTSILKVPAMPSLKNKQYQHLYTPTGDIANHLSTAVDLHP 300
 |||||||
 Db 241 ehqyvvasittrldvtsilkvampslknkqyqhlyptlgtgdiiahlsvtaldhlp 300

QY 301 TPALGVPREALYIATHEKTPRGLEFAGPIGYFTADNSEEYVGIKSMYVNOTQRATL 360
 |||||||
 Db 301 tpalgvpreaalyiathektrpgrlfgaplgiftadnsgefvvgiksmynvnotqrratl 360

QY 361 FAGAGIVADSDAQOEYETGKFEPMROLKDYNHVE 397
 |||||||
 Db 361 fagagivadsdaqeeyetgkfkfemrqllkdynhve 397

RESULT 2
 AAB08635 standard; Protein: 397 AA.

AC AAB08635;
 DT 20-DEC-2000 (first entry)
 DE Amino acid sequence of a human neutral sphingomyelinase (N-SMase).
 XX Human: neutral sphingomyelinase; N-SMase; anti-lipemic drug; SREBP-1;
 KM sterol regulatory element binding protein-1; serum cholesterol; betaAPP;
 KM LDL receptor; fatty acid synthesis; amyloid precursor protein; obesity;
 KM hyperlipoproteinemia; hypercholesterolemia; stroke; obesity; cirrhosis;
 KM cardiac disease; atherosclerosis; cerebral atherosclerosis;
 KM cholesterol ester storage disorder; organ transplantation failure;
 KM viral infection; encephalitis; liver disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200050574-A1.
 PD 31-AUG-2000.
 XX
 PD 23-FEB-2000; 2000MO-US04657.
 PF 24-FEB-1999; 99US-0121447.
 PR 24-FEB-1999; 99US-0121447.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Chatterjee S;
 XX
 DR WPI; 2000-572085/53.
 DR N-PSDB; AAA64396.
 XX
 XX Anti-lipemic drug comprising an effector of sterol regulatory element
 PT binding protein-1 for treating hyperlipoproteinemia, stroke, obesity,
 PT atherosclerosis, organ transplantation failure and cirrhosis

XX Disclosure; Fig 12; 85pp; English.
 PS
 XX The present sequence represents human neutral sphingomyelinase (N-SMase)
 CC polypeptide. The polypeptides, or its fragments, is used to produce the
 CC anti-lipemic drugs of the invention. These drugs comprise at least one
 CC effector of sterol regulatory element binding protein-1 (SREBP-1). The
 CC drugs are useful for modulating serum cholesterol level, SREBP-1 level,
 CC LDL receptor level, fatty acid synthesis and production of amyloid
 CC precursor protein (betaAPP) in a mammal. They are used for the treatment
 CC of hyperlipoproteinemia including hypercholesterolemia, stroke, obesity,
 CC cardiac disease, including atherosclerosis, cerebral atherosclerosis,
 CC cholesterol ester storage disorder, liver disease, including organ
 CC transplantation failure and cirrhosis, diseases of the biliary system
 CC or viral infection facilitating encephalitis. The drugs are useful for
 CC treating disorders associated with high serum cholesterol levels in a
 CC mammal.
 XX
 SQ Sequence 397 AA;

Query Match 100.0%; Score 397; DB 21; Length 397;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTYHETRALAQSDDLQDLVALETTERGAYFAPPADTLRFGIGAITAKTAALOGAVF 60
 |||||||
 Db 1 mmythetralaqsdlqdlvaaleetefgayfapaddtlrfgigataktakagavf 60

QY 61 GAOSFDEQEPSEELMGFVPEVMTIADKTFEGSDIVSDPTTWLAQFVPRQPTVT 120
 |||||||
 Db 61 gagsfdeqepseelmagfvpewmvtiaadkltfsgdsvsdlttwlaqfvpkqptvt 120

QY 121 TSHVTDEVDNIERTENLIDTLAIDQTLAKVVFGRQOTLQSDTLRLAQIIRALAEQANTY 180
 |||||||
 Db 121 tshvtdevdnterentlidlalidqtlakvfvgrqqlqsdltlrlaqiiralaeganty 180

QY 181 HVLKRNDELFIATPRLVAMSGGIATAVAGTSRRGTGADIALGELLASQKNRI 240
 |||||||
 Db 181 hvltkrdelfiatprrlvamsggiataavagtsrrgtgdadialgellalsqknri 240

QY 241 EHQYVVASITTRLODVTSILKVPAMPSLKNKQYQHLYTPTGDIANHLSTAVDLHP 300
 |||||||
 Db 241 ehqyvvasittrldvtsilkvampslknkqyqhlyptlgtgdiiahlsvtaldhlp 300

QY 301 TPALGVPREALYIATHEKTPRGLEFAGPIGYFTADNSEEYVGIKSMYVNOTQRATL 360
 |||||||
 Db 301 tpalgvpreaalyiathektrpgrlfgaplgiftadnsgefvvgiksmynvnotqrratl 360

QY 361 FAGAGIVADSDAQOEYETGKFEPMROLKDYNHVE 397
 |||||||
 Db 361 fagagivadsdaqeeyetgkfkfemrqllkdynhve 397

RESULT 3
 AAY42118 standard; Protein: 92 AA.

ID AAY42118
 AC AAY42118;
 DT 13-DEC-1999 (first entry)
 DE wheat anthranilate synthase alpha subunit portion protein sequence.
 XX
 XX Anthranilate synthase alpha subunit; tryptophan biosynthetic enzyme;
 KM chimeric gene; corn; rice; soybean; wheat; tryptophan synthase;
 KM anthranilate synthase beta subunit; herbicide; fungicide; phenol type;
 KM pathogen attack; identification; transgenic plant; ASAS; ASBS; TSAS;
 KM plant breeding.
 XX
 OS Triticum aestivum.
 XX
 PN WO9949056-A2.

XX 30-SEP-1999.
 PD
 XX
 PF 19-MAR-1999; 99WO-US06046.
 XX
 PR 26-MAR-1998; 98US-0079386.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Vollmer SJ, Falco SC, Broglie RM, Bryan GT, Cahoon RE;
 PI Rafalski JA;
 XX
 DR WPI; 1999-580451/49.
 DR N-PSDB; AA25115.
 XX
 PT New isolated tryptophan biosynthetic enzyme nucleic acids, used to
 PT produce plants with altered tryptophan levels and for developing
 PT herbicides or fungicides -
 XX
 PS Claim 21; Page 64; 83pp; English.
 XX
 CC The present invention describes isolated anthranilate synthase alpha-
 CC subunit (ASAS), anthranilate synthase beta-subunit (ASBS), and
 CC tryptophan synthase alpha-subunit (TSAS) nucleic acids, and protein
 CC encoded by them, obtained from corn, rice, soybean and wheat cDNA
 CC libraries. The nucleic acid fragments may be used to create transgenic
 CC plants in which the disclosed ASAS, ASBS or TSAS are present at higher or
 CC lower levels than normal or in cell types or developmental stages in
 CC which they are not normally found. This would have the effect of altering
 CC the level of tryptophan in those cells. Manipulation of the levels of
 CC some of the ASASs will also results in changes in the response to
 CC pathogen attack. Because this pathway is not followed for the production
 CC of tryptophan in higher animals, these enzymes are very good candidates
 CC for the discovery of herbicides and fungicides. The ASAS, ASBS or TSAS
 CC can be used as targets to facilitate design and/or identification of
 CC inhibitors of those enzymes that may be useful as herbicides. Nucleic
 CC acid fragments can also be used as probes for genetically and physically
 CC mapping the genes that they are a part of, and as markers for traits
 CC linked to those genes. Such information may be useful in plant breeding
 CC in order to develop lines with desired phenotypes. AA25109 to AA25127
 CC represent specifically claimed nucleic acids from the present invention
 CC and AA42112 to AA42130 represent the proteins encoded by them.
 XX
 SQ Sequence 92 AA;
 Query Match 2.3%; Score 9; DB 20; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 362 AGAGIVADS 370
 Db 53 agegIvads 61
 RESULT 4
 AA42113
 ID AA42113 standard; Protein; 446 AA.
 XX
 AC AA42113;
 XX
 DT 13-DEC-1999 (first entry)
 XX
 DE Corn anthranilate synthase alpha subunit portion protein sequence.
 XX
 KW Anthranilate synthase alpha subunit; tryptophan biosynthetic enzyme;
 KW chimeric gene; corn; rice; soybean; wheat; tryptophan synthase;
 KW anthranilate synthase beta subunit; herbicide; fungicide; phenotype;
 KW pathogen attack; identification; transgenic plant; ASAS; ASBS; TSAS;
 KW plant breeding.
 XX
 OS Zea mays.
 XX

FH Key Location/Qualifiers
 FT Misc-difference 31
 FT /note="unspecified"
 XX
 PN WO9949058-A2.
 XX
 PD 30-SEP-1999.
 XX
 PF 19-MAR-1999; 99WO-US06046.
 XX
 PR 26-MAR-1998; 98US-0079386.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Vollmer SJ, Falco SC, Broglie RM, Bryan GT, Cahoon RE;
 PI Rafalski JA;
 XX
 DR WPI; 1999-580451/49.
 DR N-PSDB; AA25110.
 XX
 PT New isolated tryptophan biosynthetic enzyme nucleic acids, used to
 PT produce plants with altered tryptophan levels and for developing
 PT herbicides or fungicides -
 XX
 PS Claim 21; Page 57-59; 83pp; English.
 XX
 CC The present invention describes isolated anthranilate synthase alpha-
 CC subunit (ASAS), anthranilate synthase beta-subunit (ASBS), and
 CC tryptophan synthase alpha-subunit (TSAS) nucleic acids, and protein
 CC encoded by them, obtained from corn, rice, soybean and wheat cDNA
 CC libraries. The nucleic acid fragments may be used to create transgenic
 CC plants in which the disclosed ASAS, ASBS or TSAS are present at higher or
 CC lower levels than normal or in cell types or developmental stages in
 CC which they are not normally found. This would have the effect of altering
 CC the level of tryptophan in those cells. Manipulation of the levels of
 CC some of the ASASs will also results in changes in the response to
 CC pathogen attack. Because this pathway is not followed for the production
 CC of tryptophan in higher animals, these enzymes are very good candidates
 CC for the discovery of herbicides and fungicides. The ASAS, ASBS or TSAS
 CC can be used as targets to facilitate design and/or identification of
 CC inhibitors of those enzymes that may be useful as herbicides. Nucleic
 CC acid fragments can also be used as probes for genetically and physically
 CC mapping the genes that they are a part of, and as markers for traits
 CC linked to those genes. Such information may be useful in plant breeding
 CC in order to develop lines with desired phenotypes. AA25109 to AA25127
 CC represent specifically claimed nucleic acids from the present invention
 CC and AA42112 to AA42130 represent the proteins encoded by them.
 XX
 SQ Sequence 446 AA;
 Query Match 2.3%; Score 9; DB 20; Length 446;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 362 AGAGIVADS 370
 Db 408 agegIvads 416
 RESULT 5
 AA42113
 ID AA42113 standard; Protein; 577 AA.
 XX
 AC AA42113;
 XX
 DT 25-JUN-1999 (first entry)
 XX
 DE Rice ASA first isozyme alpha-subunit protein variant.
 XX
 KW Anthranilate synthase; alpha-subunit; ASA; rice; isozyme; plant; seed;
 KW maize; wheat; tryptophan content; nutritional value.
 XX

Query Match 2.3%; Score 9; DB 18; Length 615;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADS 370
 |||||||
 Db 576 agagivads 584

RESULT 10
 AAW26686
 ID AAW26686 standard; Protein; 615 AA.
 AC AAW26686;
 DT 27-MAR-1998 (first entry)
 DE Maize anthranilate synthase alpha subunit.
 KW Anthranilate synthase; L-tryptophan; tolerance; resistance;
 KM transgenic plant; maize; selectable marker.
 OS Zea mays inbred line Va26.
 FT Key Location/Qualifiers
 FT Peptide 1..46 /label=Transit_peptide
 MO9726366-A1.
 PD 24-JUL-1997.
 PF 17-JAN-1997; 97MO-US00983.
 PR 19-JAN-1996; 96US-0604789.
 PA (DEKA-) DEKALB GENETICS CORP.
 PI Anderson PC, Chomet PS, Griffior MC, Kriz AL;
 DR N-PSDB; AAT91103.
 DR WPI; 1997-385350/35.
 DR N-PSDB; AAT91103.
 PT DNA encoding anthranilate synthase resistant to inhibition by
 PT tryptophan - and transformed plants, used e.g. to improve tryptophan
 PT levels in plants and as marker for cell selection
 PS Claim 7; Fig 3; 87pp; English.
 XX This protein sequence comprises a maize anthranilate synthase (AS)
 CC alpha subunit encoded by a cDNA clone (see AAT91103) obtained from
 CC inbred line Va26. It differs at only 1 residue (Met-377 for Lys)
 CC from the alpha subunit (see AAW26685) of a maize allele C28 AS that
 CC is resistant to inhibition by free L-tryptophan or its amino acid
 CC analogues. Maize AS sequences, especially those from the C28
 CC allele, can be used in claimed methods: (i) to impart tolerance of
 CC plants to tryptophan; (ii) to alter, particularly increase, the
 CC tryptophan content of plants, either to increase nutritional value or as a
 CC source of tryptophan for extraction; (iii) for production of recombinant AS
 CC (used for screening to identify agents that bind to or inhibit it);
 CC and (iv) for selection of transformed cells. Transgenic plants
 CC containing AS can be used for production of proteins or other
 CC compounds, including in vitro culture of their cells. The trait of
 CC resistance to tryptophan can be introduced to a wide variety of commercial
 CC maize lines.
 XX
 SO Sequence 615 AA;

Query Match 2.3%; Score 9; DB 18; Length 615;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 362 AGAGIVADS 370
 |||||||
 Db 576 agagivads 584

RESULT 11
 AAY33698
 ID AAY33698 standard; Protein; 271 AA.
 AC AAY33698;
 DT 14-JAN-2000 (first entry)
 DE E. coli entc protein fragment.
 KW Isochorismate synthase; ICS; plant; pathogen resistance; chitinase;
 KM pathogen inducible promoter; antipathogenic protein; toxin; entc;
 KM antifungal protein; albumin-type protein; hypersensitive response,
 XX Escherichia coli.
 OS WO9950423-A2.
 PN 07-OCT-1999.
 PD 25-MAR-1999; 99WO-EP02176.
 PF 31-MAR-1998; 98US-0080203.
 PR 03-APR-1998; 98US-0080625.
 PA (MOGE-) MOGEN INT NV.
 PA (UYLE-) RIJKSUNIV LEIDEN.
 PA (UYNI-) UNIV NIJMEGEN.
 PI Lanthorst HJM, Verpoorte R, Verberne MC, Moreno PR;
 PI Van Tegelen LJP, Willems GJ, Croes AF, Stuijver MH, Custers J;
 PI Simons LH, Melchers LS, Bol JF;
 DR WPI; 1999-610856/52.
 DR N-PSDB; AAZ23756.
 DR
 PT Method for inducing pathogen resistance in plants -
 PS Example 3; Page 53-54; 66pp; English.
 XX This invention describes a novel method for the induction of pathogen
 CC resistance in plants, by transformation with an expression cassette
 CC harboring a gene coding for an isochorismate synthase (ICS). A pathogen
 CC inducible promoter can be used to drive expression of a heterologous
 CC protein. The heterologous protein used in the method of the invention is
 CC an antipathogenic protein e.g. chitinase, glucanase, osmotin, lectins,
 CC saccharide oxidase, oxalate oxidase, magainins, toxins from Bacillus
 CC thuringiensis, or antifungal proteins isolated from Mirabilis jalapa,
 CC Amaranthus, Raphanus, Brassica, Sinapis, Arabidopsis, Dahlia, Citrus,
 CC Lathyrus, Ciceraria, Allium seeds, Atralia and Impatiens and albumin-type
 CC proteins, such as thionin, napin, barley trypsin inhibitor, cereal
 CC gliadin and wheat-alpha-amylase, or a protein that can induce a
 CC hypersensitive response, such as Cf, Bs3 and Po proteins from tomato and
 CC N-protein from tobacco. This sequence encodes the Escherichia coli
 CC isochorismate synthase entc gene which is described in the method of
 CC the invention.
 XX
 SO Sequence 271 AA;

Query Match 2.0%; Score 8; DB 20; Length 271;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 360 LFAGAGIV 367
 |||||||
 Db 238 lfagagiv 245

RESULT 12

AAB08519
ID AAB08519 standard; Protein: 287 AA.

XX
AC AAB08519;

DT 20-DEC-2000 (first entry)

XX Protein encoded by haemoglobin-response gene HBR2.

DE Haemoglobin-response gene; HBR1; HBR2; HBR3; haemoglobin; adhesion;

KW disseminated infection; blastococidia; fibronectin.

XX Candida albicans.

OS WO200050601-A2.

XX 31-AUG-2000.

XX 18-JAN-2000; 2000MO-US01184.

XX 26-FEB-1999; 99US-0258634.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Roberts DD, Yan S;

DR WPI; 2000-543913/49.

XX Detecting disseminated Candida albicans infections using
PT hemoglobin-response genes and proteins, probes and antibodies derived
PT from them -

XX Claim 3; Page 50-51; 54pp; English.

XX The present sequence is encoded by a haemoglobin-response gene HBR2 from
CC Candida albicans. The specification also describes haemoglobin-response
CC genes HBR1 and HBR3. The expression of these genes is specifically
CC induced when the organism is exposed to haemoglobin during disseminated
CC infections. Haemoglobin induces increased adhesion of C. albicans
CC blastococidia to fibronectin. HBR1, HBR2 and HBR3 nucleic acid probes,
CC proteins and antibodies are used for the diagnosis of disseminated
CC C. albicans infections.

XX Sequence 287 AA;

Query Match 2.0%; Score 8; DB 21; Length 287;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GATPATPA 35

Db 248 gayfatpa 255

RESULT 13

AAM00815
ID AAM00815 standard; Protein: 313 AA.

XX
AC AAM00815;

DT 01-OCT-2001 (first entry)

XX Human bone marrow protein, SEQ ID NO: 178.

DE Human; bone marrow; antiinflammatory; cytosolic; neuroprotective;

KW antiviral; antibacterial; antifungal; anti-HIV; haemostatic;

KM immunosuppressive; gene therapy; cytokine cell proliferation;
KW cell differentiation modulator; immune disorder; infection; cancer;
XX human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.

OS Homo sapiens.

XX WO200153453-A2.

XX 26-JUL-2001.

XX 23-DEC-2000; 2000MO-US34960.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0598042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

XX 30-NOV-2000; 2000US-0250583.

XX (HYSE-) HYSEQ INC.

XX Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;

XX Ren F, Wang J, Werhman F, Xu C, Xue AJ, Yang Y, Zhang J;

XX Zhao QA, Zhou P, Drmanac RT;

XX WPI; 2001-488707/53.

XX N-PDB; AAH89934.

XX Claim 10; Page 334-335; 648pp; English.

XX The present sequence is one of 251 novel human polypeptides encoded
CC by a bone marrow-expressed polynucleotide. The polynucleotide and the
CC polypeptide encoded by it are useful in the treatment of various
CC immune deficiencies and disorders. The deficiencies and disorders may
CC be genetic, or may be caused by a viral (e.g. HIV), bacterial or fungal
CC infection, or may result from an autoimmune disorder, a coagulation
CC disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
CC suppression of an inflammatory response or treatment of a nervous
CC system disorder such as Alzheimer's disease. Detection of the presence
CC or increased expression of the polynucleotide or the protein it
CC encodes is useful for the diagnosis and/or prognosis of one
CC or more types of cancer. The polynucleotide and polypeptide can be
CC used as nutritional sources or supplements and in the screening of
CC chemical compounds as potential drugs.

XX Sequence 313 AA;

Query Match 2.0%; Score 8; DB 22; Length 313;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 VEGRQOTL 158

Db 157 vfgrqtl 164

RESULT 14

AAV50338
ID AAV50338 standard; Protein: 331 AA.

XX
AC AAV50338;

DT 14-JAN-2000 (first entry)

XX P. fluorescens ICS orfA protein fragment.

DE Isochorismate synthase; ICS; plant; pathogen resistance; chitinase;

KW pathogen inducible promoter; antipathogenic protein; toxin;

KM antifungal protein; albumin-type protein; hypersensitive response.
XX Pseudomonas fluorescens.

XX W09950423-A2.
PN 07-OCT-1999.
XX
XX
XX 25-MAR-1999; 99WO-EP02176.
PF
XX 31-MAR-1998; 98US-0080203.
PR 03-APR-1998; 98US-0080625.
XX
XX (MOGE-) MOGEN INT NV.
PA (UYLE-) RIJSUNTV LEIDEN.
PA (UYNI-) UNIV NIMEGEN.
XX
XX Linthorst HJM, Verpoorte R, Verberne MC, Moreno PRH;
PI Van Tegelen LJP, Willems GJ, Croes AF, Stuiver MH, Custers J;
PI Simons LH, Melchers LS, Bol JF;
XX
XX WPI: 1999-610856/52.
DR N-PSDB; AA223757.
XX
XX Method for inducing pathogen resistance in plants -
PT
XX
XX Example 3; Page 58-59; 66pp; English.
PS
XX This invention describes a novel method for the induction of pathogen
CC resistance in plants, by transformation with an expression cassette
CC harboring a gene coding for an isochorismate synthase (ICS). A pathogen
CC inducible promoter can be used to drive expression of a heterologous
CC protein. The heterologous protein used in the method of the invention is
CC an antipathogenic protein e.g. chitinase, glucanase, osmotin, lectins,
CC saccharide oxidase, oxalate oxidase, magainins, toxins from *Bacillus*
CC *thuringeriensis*, or antifungal proteins isolated from *Mirabilis jalapa*,
CC *Amaranthus*, *Raphanus*, *Brassica*, *Sinapis*, *Arabidopsis*, *Dahlia*, *Galins*,
CC *Lathyrus*, *Clitoria*, *Allium* seeds, *Aralia* and *Impatiens* and albumin-type
CC proteins, such as thionine, napin, barley trypsin inhibitor, cereal
CC gliadin and wheat-alpha-amylase, or a protein that can induce a
CC hypersensitive response, such as Cf, Bs3 and Po proteins from tomato and
CC N-protein from tobacco. This sequence represents a pseudomonas
CC fluorescens isochorismate synthase orfa protein fragment which is
CC described in the method of the invention.
XX
XX Sequence 331 AA;
SQ

Query Match 2.0%; Score 8; DB 20; Length 331;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 LFAGAGIV 367
DB 297 lftagagiv 304
|||||

RESULT 15
AAV50335
ID AAV50335 standard; Protein: 391 AA.
XX
AC AAV50335;
XX
DT 14-JAN-2000 (first entry)
XX
DE E. coli entc protein.
XX

XX Isochorismate synthase; ICS; plant; pathogen resistance; chitinase;
KW pathogen inducible promoter; antipathogenic protein; toxin; entc;
KW antifungal protein; albumin-type protein; hypersensitive response.
XX
OS *Escherichia coli*.
XX
XX W09950423-A2.
PN
XX
PD 07-OCT-1999.

XX 25-MAR-1999; 99WO-EP02176.
PF
XX 31-MAR-1998; 98US-0080203.
PR 03-APR-1998; 98US-0080625.
XX
XX (MOGE-) MOGEN INT NV.
PA (UYLE-) RIJSUNTV LEIDEN.
PA (UYNI-) UNIV NIMEGEN.
XX
XX Linthorst HJM, Verpoorte R, Verberne MC, Moreno PRH;
PI Van Tegelen LJP, Willems GJ, Croes AF, Stuiver MH, Custers J;
PI Simons LH, Melchers LS, Bol JF;
XX
XX WPI: 1999-610856/52.
DR N-PSDB; AA223756.
XX
XX Method for inducing pathogen resistance in plants -
PT
XX
XX Example 3; Page 51-53; 66pp; English.
PS
XX This invention describes a novel method for the induction of pathogen
CC resistance in plants, by transformation with an expression cassette
CC harboring a gene coding for an isochorismate synthase (ICS). A pathogen
CC inducible promoter can be used to drive expression of a heterologous
CC protein. The heterologous protein used in the method of the invention is
CC an antipathogenic protein e.g. chitinase, glucanase, osmotin, lectins,
CC saccharide oxidase, oxalate oxidase, magainins, toxins from *Bacillus*
CC *thuringeriensis*, or antifungal proteins isolated from *Mirabilis jalapa*,
CC *Amaranthus*, *Raphanus*, *Brassica*, *Sinapis*, *Arabidopsis*, *Dahlia*, *Galins*,
CC *Lathyrus*, *Clitoria*, *Allium* seeds, *Aralia* and *Impatiens* and albumin-type
CC proteins, such as thionine, napin, barley trypsin inhibitor, cereal
CC gliadin and wheat-alpha-amylase, or a protein that can induce a
CC hypersensitive response, such as Cf, Bs3 and Po proteins from tomato and
CC N-protein from tobacco. This sequence represents the *Escherichia coli*
CC isochorismate synthase entc gene which is described in the method of
CC the invention.
XX
XX Sequence 391 AA;
SQ

Query Match 2.0%; Score 8; DB 20; Length 391;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 LFAGAGIV 367
DB 358 lftagagiv 365
|||||

Search completed: March 27, 2002, 15:39:37
Job time: 293 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 27, 2002, 15:34:44 ; Search time 12.6 seconds
(without alignments)
709.032 Million cell updates/sec

Title: US-08-774-104A-2
Perfect score: 397
Sequence: 1 MMTYHETRALAQSDLOQLYA.....ETGLKPEPMQLKDYNHVE 397

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 8

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents, AA:*

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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCRTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	397	100.0	397	2	US-08-774-104A-2
2	9	2.3	604	3	US-08-604-789B-2
3	9	2.3	604	3	US-08-604-789B-16
4	9	2.3	604	4	US-09-312-721A-2
5	9	2.3	604	4	US-09-312-721A-16
6	9	2.3	621	4	US-08-604-789B-4
7	9	2.3	621	4	US-09-312-721A-4
8	8	2.0	616	2	US-09-001-826-5

ALIGNMENTS

RESULT 1
US-08-774-104A-2
; Sequence 2, Application US/08774104A
; Patent No. 5919687
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Subroto
; TITLE OF INVENTION: RECOMBINANT N-SMASES AND NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA

COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,104A
FILING DATE: 12/24/96
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46906
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-774-104A-2

Query Match 100.0%; Score 397; DB 2; Length 397;
Best Local Similarity 100.0%; Pred No. 0;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMTYHETRALAQSDLOQLYALETTERGAYFATPADDTLRFGIGALATATAQAAGAVF 60
DB 1 MMTYHETRALAQSDLOQLYALETTERGAYFATPADDTLRFGIGALATATAQAAGAVF 60
QY 61 GAOSFDEQETPQSELNAGFVPEVWVTIAADKITFGSDTVSPFTWLAOFVKOPNTVT 120
DB 61 GAOSFDEQETPQSELNAGFVPEVWVTIAADKITFGSDTVSPFTWLAOFVKOPNTVT 120
QY 121 TSHVTEVDMDIERENTIDFLAIDOTLAKVYFGROOTLQSDPLRLAQIIRALAEQANTY 180
DB 121 TSHVTEVDMDIERENTIDFLAIDOTLAKVYFGROOTLQSDPLRLAQIIRALAEQANTY 180
QY 181 HVLKRHDELFIATPERLVAMSGGQATATAVAGTSRGTGADADIALGALLASQKNRI 240
DB 181 HVLKRHDELFIATPERLVAMSGGQATATAVAGTSRGTGADADIALGALLASQKNRI 240
QY 241 EHOYVVASITTRLODVTTSIKVPAMPSLKNKQYOHLYTPTGDIANHLSTVAIVDLHP 300
DB 241 EHOYVVASITTRLODVTTSIKVPAMPSLKNKQYOHLYTPTGDIANHLSTVAIVDLHP 300
QY 301 TPALGVPREALAYITATHEKTRPGFLGAGPIGTADNSGEFVYVIGISMYNOTORATL 360
DB 301 TPALGVPREALAYITATHEKTRPGFLGAGPIGTADNSGEFVYVIGISMYNOTORATL 360
QY 361 FAGAGIVADSDAQOEYETGLKPEPMQLKDYNHVE 397
DB 361 FAGAGIVADSDAQOEYETGLKPEPMQLKDYNHVE 397
RESULT 2
US-08-604-789B-2
; Sequence 2, Application US/08604789B
; Patent No. 6118047

GENERAL INFORMATION:
APPLICANT: Anderson, P.C.
Chomet, P.S.
Griffor, M.C.
Kriz, A.L.
TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
OVERPRODUCTION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,789B
FILING DATE: 19-Jan-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.026US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6903
TELEFAX: (612) 339-3061
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-604-789B-2

Query Match 2.3%; Score 9; DB 3; Length 604;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
|||||
Db 565 AGAGIVADS 573

RESULT 3
US-08-604-789B-16
Sequence 16, Application US/08604789B
Patent No. 6118047
GENERAL INFORMATION:
APPLICANT: Anderson, P.C.
Chomet, P.S.
Griffor, M.C.
Kriz, A.L.
TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
OVERPRODUCTION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN

COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,789B
FILING DATE: 19-Jan-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.026US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6903
TELEFAX: (612) 339-3061
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-08-604-789B-16

Query Match 2.3%; Score 9; DB 3; Length 604;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
|||||
Db 565 AGAGIVADS 573

RESULT 4
US-09-312-721A-2
Sequence 2, Application US/09312721A
Patent No. 6271016
GENERAL INFORMATION:
APPLICANT: Anderson, P.C.
Chomet, P.S.
Griffor, M.C.
Kriz, A.L.
TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
OVERPRODUCTION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,721A
FILING DATE: 17-May-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/604,789
FILING DATE: 19-Jan-1996
ATTORNEY/AGENT INFORMATION:

```

; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 950.026US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6903
; TELEFAX: (612) 339-3061
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 604 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-312-721A-2

Query Match
Best Local Similarity 100.0%; Score 9; DB 4; Length 604;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
Db 565 AGAGIVADS 573

RESULT 5
US-09-312-721A-16
; Sequence 16, Application US/09312721A
; Patent No. 6271016
; GENERAL INFORMATION:
; APPLICANT: Anderson, P.C.
; Chomet, P.S.
; Griffor, M.C.
; Kriz, A.L.
; TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
; AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
; OVERPRODUCTION
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312.721A
; FILING DATE: 17-May-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/604,789
; FILING DATE: 19-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 950.026US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6903
; TELEFAX: (612) 339-3061
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 604 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-312-721A-16

Query Match
Best Local Similarity 100.0%; Score 9; DB 4; Length 604;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
Db 565 AGAGIVADS 573

RESULT 6
US-08-604-789B-4
; Sequence 4, Application US/08604789B
; Patent No. 6118047
; GENERAL INFORMATION:
; APPLICANT: Anderson, P.C.
; Chomet, P.S.
; Griffor, M.C.
; Kriz, A.L.
; TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
; AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
; OVERPRODUCTION
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,789B
; FILING DATE: 19-Jan-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 950.026US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6903
; TELEFAX: (612) 339-3061
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 621 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-604-789B-4

Query Match
Best Local Similarity 100.0%; Score 9; DB 3; Length 621;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
Db 570 AGAGIVADS 578

RESULT 7
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US-09-312-721A-4
; Sequence 4, Application US/09312721A
; Patent No. 6271016
; GENERAL INFORMATION:
; APPLICANT: Anderson, P.C.
; Chomet, P.S.
; Griffor, M.C.
; Kriz, A.L.
; TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
; AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
; OVERPRODUCTION
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,721A
; FILING DATE: 17-May-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/604,789
; FILING DATE: 19-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 950,026US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6903
; TELEFAX: (612) 339-3061
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 621 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-312-721A-4

Query Match 2.3%; Score 9; DB 4; Length 621;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
Db 570 AGAGIVADS 578

RESULT 8
US-09-001-826-5
; Sequence 5, Application US/09001826A
; Patent No. 5965727
; GENERAL INFORMATION:
; APPLICANT: SONG, HEE-SOOK
; APPLICANT: BROTHERTON, JEFFREY E.
; APPLICANT: WIDHOLM, JACK M.
; TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE
; FILE REFERENCE: 01001.C1
; CURRENT APPLICATION NUMBER: US/09/001,826A
; CURRENT FILING DATE: 1997-12-31
; EARLIER APPLICATION NUMBER: 08/937,739; 60/025,140
; EARLIER FILING DATE: 1997-07-25; 1996-07-26

; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Macintosh Wordperfect converted to PC ASCII Text
; SEQ ID NO 5
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-001-826-5

Query Match 2.0%; Score 8; DB 2; Length 616;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 GAGIVADS 370
Db 543 GAGIVADS 550

Search completed: March 27, 2002, 15:39:05
Job time: 261 sec

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